

19. Analyze the BLAST algorithm, covering its features, categories and practical applications.
20. Explore Structural Genomics, detailing its significance, associated tools and real-world applications.

APRIL/MAY 2025

**23USBC43 — BIOINFORMATICS (SEC VI)**

Time : Three hours

Maximum : 75 marks



**SECTION A — (10 × 2 = 20 marks)**

Answer ALL questions.

1. Differentiate between Genomics and Transcriptomics.
2. Define Metabolic Database with an example.
3. State the purpose of the SwissProt database.
4. List two types of Sequence Alignment methods.
5. Mention the main feature of the RASMOL tool.
6. Define Nutrigenomics and highlight its significance.
7. Differentiate between PAM and BLOSUM matrices.
8. Name two BLAST algorithms.



9. Describe the purpose of the VISTA server.

10. Define Comparative Genomics.

SECTION B — (5 × 5 = 25 marks)

Answer ALL questions.

11. (a) Explain the concept of Genome and its applications.

Or

(b) Describe the features and types of Metabolic Databases.

12. (a) Explain the Needleman-Wunsch algorithm for Global Sequence Alignment.

Or

(b) Describe the procedure and applications of DNA Microarray.

13. (a) Explain the concept of Molecular Visualization and its tools.

Or

(b) Describe the different types of Sequence Alignment methods.



14. (a) Explain the concept of Structural Genomics and its applications.

Or

(b) Describe the features and applications of the KEGG database.

15. (a) Explain the concept of Comparative Genomics and its tools.

Or

(b) Describe the features and applications of the PDB database.

SECTION C — (3 × 10 = 30 marks)

Answer any THREE questions.

16. Elaborate on the concept of Bioinformatics, highlighting its key applications.

17. Discuss various types of Biological Databases, emphasizing their characteristics and providing relevant examples.

18. Examine Sequence Alignment by explaining its significance, classification and commonly used methods.